

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
 - (ii) TITLE OF INVENTION: CHIMERIC GENES AND

 METHODS FOR INCREASING
 INCREASING THE LYSINE
 AND THREONINE CONTENT
 OF THE SEEDS OF PLANTS
 - (iii) NUMBER OF SEQUENCES: 107
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS
 AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 19898
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: MICROSOFT WORD VERSION 2.0C
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BARBARA C. SIEGELL
 - (B) REGISTRATION NUMBER: 30,684
 - (C) REFERENCE/DOCKET NUMBER: BB-1037-C
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 302-992-4931
 - (B) TELEFAX: 302-773-0164
 - (C) TELEX: 835420

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1350
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT

 Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp

 1 5 10 15
- TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC

 Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn

 20 25 30
- GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG 144
 Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
 35 40 45
- GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC 192
 Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
 50 55 60
- GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC

 Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr

 65 70 75 80
- CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT

 Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr

 85

 90

 95
- GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT

 Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp

 100 105 110
- GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GAT GAG 384
 Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
 115 120 125
- ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA 432

 Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys

 130 135 140
- GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC

 Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala

 145

 150

 150

 160
- GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA 528 Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu

			165				170				175		
								GAA Glu					576
								ACG Thr					624
								TGG Trp 220					672
								GCA Ala					720
								GCA Ala					768
								GTA Val					816
								GCA Ala					864
								CGC Arg 300					912
								CTG Leu					960
								CTC Leu					1008
			Leu				Glu				Leu	ACC Thr	1056
		Thr				Thr				Leu		CAA Gln	1104
	Leu				Ala				Glu			GAA Glu	1152
Leu				Leu				Leu				TGC Cys 400	1200

	GTT Val														1248
	ATT Ile														1296
	GAA Glu														1344
GAG Glu	TAA * 450														1350
(2)	II	NFORI	MATI	ON F	OR SI	EQ II	O NO	:2:			•				
		(i)	(A) (B) (C) (D)	L: T S' T(E CHA ENGTI YPE: TRANI OPOLO	H: : nuc DEDNI DGY:	36 bacleio ESS: lia	ase j c ac: sin	pair: id ngle						
		(ii) MOLECULE TYPE: DNA (genomic)													
	(:	xi)	SEQ.	UENC	E DE:	SCRI:	PTIO	N:	SEQ	ID N	0:2:				
GAT	CCAT	GGC '	TGAA.	ATTG	TT G'	rctc(CAAA'	T TT	GGCG				3	6	
(2)	I	NFOR	ITAM	ON F	OR S	EQ I	D NO	:3:							
		(i)	SEQ (A) (B) (C) (D)	L T S	E CH. ENGT: YPE: TRAN: OPOL	H: nu DEDN	36 b clei ESS:	ase c ac si	pair id ngle						
	(ii)	MOL	ECUL	Е ТҮ	PE:	DNA	(ge	nomi	c)					
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N:	SEQ	ID N	0:3:				
GTA	.ccgc	CAA	ATTT	GGAG	AC A	ACAA	TTTC	A GC	CATG				3	6	
(2)	I	NFOR	MATI	ON F	OR S	EQ I	D NO	:4:							
		(i)	SEQ (A) (B) (C) (D)	L T S	E CH ENGT YPE: TRAN	H: nu DEDN	48 b clei ESS:	ase c ac	pair id ngle						
	(ii)	MOL	ECUL	E TY	PE:	DNA	. (ge	nomi	c)					
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N:	SEQ	ID N	0:4:				
CCC	:GGGC	CAT	GGCT	'ACAG	GT T	TAAC	AGCT	'A AG	ACCG	GAGT	AGA	.GCAC	T 4	8	

	(SEQU (A) (B) (C) (D)	LE TY ST	CHA NGTH PE: RAND POLO	: 3 nuc EDNE	7 ba leic SS:	se p aci sin	airs d					
	(i	i)	MOLE	CULE	TYP	Ε:	DNA	(gen	omic)				
	(x	i)	SEQU	ENCE	DES	CRIP	TION	: s	EQ I	D NO	:5:			
GATA	TCGA	AT T	CTCA	TATT	A GA	ACTC	CAGC	TTT	TTTC			37		
(2)	IN	FORM	OITA	N FO	R SE	Q ID	NO:	6:						
	(i)	SEQU (A) (B) (C) (D)	LE TY ST	CHA NGTH PE: RAND	: 9 nuc EDNE	17 b leic	ase aci	pair	's				
	(i	i)	MOLE	CULE	TYP	E:	DNA	(gen	omic	:)				
	(i	.x)	FEAT (A) (B)	NA	ME/K			; 911						
	(×	i)	SEQU	JENCE	DES	CRIF	MOIT	J: S	EQ I	D NC):6:			
	ATG G Met A													47
	GTT Val													95
	ATC Ile													143
	GAT Asp													191
	GCC Ala 65													239
	GAT Asp													287
	TCT Ser													335

(2) INFORMATION FOR SEQ ID NO:5:

							GGA Gly		383	
							ATT Ile		431	
							GAT Asp		479	
							GAC Asp	_	527	
							GGA Gly 190		575	
							GCT Ala		623	
							ACA Thr		671	
						_	CGT Arg	_	719	
							GGT Gly		767	
						_	GGC Gly 270	_	815	
							CAG Gln	_	863	
					GGA Gly		TAA *	TGAG	AATTC	91

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:7:		
CTTCCCGTGA CCA	ATGGGCCA TC	22	
(2) INFORMAT	TION FOR SEQ ID NO:8:		
(<i>p</i> (E	EQUENCE CHARACTERISTICS: A) LENGTH: 75 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear		
(ii) MC	OLECULE TYPE: DNA (genomic)		
(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:8:		
CATGGCTGGC TTC	CCCCACGA GGAAGACCAA CAATGACATT ACCTCCATTG	G CTAGCAACGG	60
TGGAAGAGTA CAA	ATG		75
(2) INFORMAT	TION FOR SEQ ID NO:9:		
(EQUENCE CHARACTERISTICS: A) LENGTH: 75 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear		
(ii) Mo	OLECULE TYPE: DNA (genomic)		
(xi) SI	EQUENCE DESCRIPTION: SEQ ID NO:9:		
CATGCATTGT ACT	TCTTCCAC CGTTGCTAGC AATGGAGGTA ATGTCATTGT	TGGTCTTCCT	60
CGTGGGGAAG CC	AGC		75
(2) INFORMA	TION FOR SEQ ID NO:10:		
(7 (1 (0	EQUENCE CHARACTERISTICS: A) LENGTH: 90 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear		
(ii) Mo	OLECULE TYPE: DNA (genomic)		
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:10:		
CATGGCTTCC TC	AATGATCT CCTCCCCAGC TGTTACCACC GTCAACCGTC	G CCGGTGCCGG	60
CATGGTTGCT CC	ATTCACCG GCCTCAAAAG		90
(2) INFORMA	TION FOR SEQ ID NO:11:		
(i) S	EQUENCE CHARACTERISTICS:		

LENGTH: 90 base pairs

TYPE: nucleic acid

(A) (B)

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:11:	
CATGCTTTTG	AGGCCGGTGA ATGGAGCAAC CATGCCGGCA CCGGCACGGT TGACGGTGGT	60
AACAGCTGGG	GAGGAGATCA TTGAGGAAGC	90
(2) INFO	RMATION FOR SEQ ID NO:12:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:12:	
CCGGTTTGCT	GTAATAGGTA CCA 23	
(2) INFO	RMATION FOR SEQ ID NO:13:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:13:	
AGCTTGGTAC	CTATTACAGC AAACCGGCAT G 31	
(2) INFO	RMATÍON FOR SEQ ID NO:14:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GCTTCCTCAA	TGATCTCCTC CCCAGCT 27	
(2) INFO	RMATION FOR SEQ ID NO:15:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs	

(B) TYPE: nucleic acid

			STRANDEDN TOPOLOGY:			le	
	(ii)	MOLECU	JLE TYPE:	DNA	(genoi	mic)	
	(xi)	SEQUE	ICE DESCRI	OITG	1: SE	Q ID	NO:15:
CATTG	TACTC	TTCCAC	CGTT GCTAG	CAA			28
(2)	INFOR	MATION	FOR SEQ I	D NO	:16:		
	(i)	(A)	ICE CHARAC LENGTH: TYPE: nu STRANDEDN TOPOLOGY:	20 ba	ase pa	irs le	
	(ii)	MOLEC	JLE TYPE:	DNA	(geno	mic)	
	(ix)	(B)	RE: NAME/KEY: LOCATION: OTHER INE	1.	.20		roduct= "synthetic oligonucleotide" /standard_name= "SM 70"
	(xi) SEQ	UENCE DESC	CRIPT	ION:	SEQ	ID NO:16:
CTGAC	TCGCT	GCGCTC	GTC				20
(2)	INFOR	MATION	FOR SEQ	ID NO	:17:		
	(i)	(A) (B) (C)	NCE CHARAC LENGTH: TYPE: nu STRANDEDM TOPOLOGY:	24 bacleia NESS:	ase pa c acid sing		
	(ii)	MOLEC	ULE TYPE:	DNA	(geno	mic)	
	(ix)	FEATU (A) (B) (D)	RE: NAME/KEY LOCATION OTHER INI	: 1.	.24		coduct= "synthetic oligonucleotide" /standard_name= "SM 71"
	(xi)	SEQUE	NCE DESCR	IPTIO	N: SE	Q II	NO:17:
TATTI	TCTCC	TTACGC	ATCT GTGC				24
(2)	INFOR	RMATION	FOR SEQ	ID NO	:18:		
	(i)	SEQUE (A) (B)	NCE CHARA LENGTH: TYPE: n	27 b	ase pa	irs	

	(ii)	MOLECU	LE TYPE:	DNA	(genom	nic)	
	(ix)	(A) (B)	E: NAME/KEY LOCATION OTHER IN	: 1	27	/pro	e oduct= "synthetic oligonucleotide" /standard_name= "SM 78"
	(xi)	SEQUEN	ICE DESCR	IPTION	: SEÇ	O ID	NO:18:
TTCATC	GATA (GCGACC	CACA CCCG	TCC			27
(2)	INFOR	MOITAN	FOR SEQ	ID NO:	19:		
	(i)	(A) (B)	ICE CHARA LENGTH: TYPE: n STRANDED TOPOLOGY	27 ba ucleio NESS:	ase pai c acid singl		
	(ii)	MOLECU	JLE TYPE:	DNA	(genor	mic)	
	(ix)	(A) (B)	RE: NAME/KEY LOCATION OTHER IN	: 1.	. 27		oduct= "synthetic oligonucleotide" /standard_name= "SM 79"
	(xi)	SEQUE	NCE DESCR	IPTIO	1: SE	Q ID	NO:19:
AATATC	GATG	CCACGA'	rgcg tccg	GCG			27
(2)	INFOR	MATION	FOR SEQ	ID NO	:20:		
	(i)	SEQUEI (A) (B) (C) (D)	NCE CHARA LENGTH: TYPE: n STRANDED TOPOLOGY	55 b uclei NESS:	ase pa		
	(ii)	MOLEC	ULE TYPE:	DNA	(geno	mic)	
	(ix)	FEATU (A) (B) (D)	RE: NAME/KEY LOCATION OTHER IN	r: 1.	sc_fea .55 TION:		oduct= "synthetic oligonucleotide" /standard_name= "SM 81"

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:20:	
CATGGAG	GAG A	AAGATGAAGG CGATGGAAGA GAAGATGAAG GCGTGATAGG TACCG	55
(2) I	NFORM	MATION FOR SEQ ID NO:21:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
((ii)	MOLECULE TYPE: DNA (genomic)	
((ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 155 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 80"	
((xi)	SEQUENCE DESCRIPTION: SEQ ID NO:21:	
AATTCGC	GTAC C	CTATCACGCC TTCATCTTCT CTTCCATCGC CTTCATCTTC TCCTC	55
(2)	INFORN	MATION FOR SEQ ID NO:22:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
((ii)	MOLECULE TYPE: protein	
	(ix)	FEATURE: (A) NAME/KEY: Protein (B) LOCATION: 114 (D) OTHER INFORMATION: /label= name	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:22:	
Ме 1	et Glı	u Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala 5 10	
(2)	INFORI	MATION FOR SEQ ID NO:23:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

21

			NAME/KEY: m LOCATION: 1	nsc_feat 21	ure	
			OTHER INFORM		/pr	oduct=
		\- ,			-	"synthetic
						oligonucleotide"
						/standard_name= "SM
						84"
(xi)	SEQUEN	CE DESCRIPTI	ON: SEQ	D	NO:23:
GATGGAG	GAG A	AGATGA	AGG C			21
(2) I	NFORM	NOITA	FOR SEQ ID N	IO:24:		
	(i)	SEQUEN	ICE CHARACTER	RISTICS:		
				base pai	rs	•
			TYPE: nucle			
			STRANDEDNESS	_	.e	
		(D)	TOPOLOGY:]	inear		
(ii)	MOLECU	JLE TYPE: DI	IA (genom	nic)	
(ix)	FEATUR	RE:			
		(A)	NAME/KEY: n	misc_feat	ure	
				121		_
		(D)	OTHER INFORM	MATION:	/pr	oduct= "synthetic oligonucleotide"
						/standard_name= "SM 85"
((xi)	SEQUEN	NCE DESCRIPT	ION: SEÇ) ID	NO:24:
ATCGCCT	TCA T	CTTCT	CCTC C			21
(2) I	NFORM	NOITAN	FOR SEQ ID 1	NO:25:		
	(i)	SEQUE	NCE CHARACTE	RISTICS:		
		(A)		base pai	irs	
		(B)		eic acid		
		(C)	STRANDEDNESS	_	Le	
		(D)	TOPOLOGY:	linear		
((ii)	MOLECU	JLE TYPE: DI	NA (genom	nic)	
((ix)	FEATU	RE:			
		(A)	NAME/KEY: 1	misc_feat	cure	2
		(B)		121		
		(D)	OTHER INFOR	: MOITAM	/pr	roduct= "synthetic
						oligonucleotide"
						/standard_name= "SM 82"
						02
•	(xi)	SEQUE	NCE DESCRIPT	ION: SEQ	ID	NO:25:

(ix) FEATURE:

GATGGAGGAG AAGCTGAAGG C

INFORMATION FOR SEQ ID NO:26: (2) SEQUENCE CHARACTERISTICS: LENGTH: 21 base pairs (A) (B) TYPE: nucleic acid (C) STRANDEDNESS: single TOPOLOGY: linear (D) (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: misc_feature LOCATION: 1..21 (B) (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26: ATCGCCTTCA GCTTCTCCTC C 21 INFORMATION FOR SEQ ID NO:27: (2) (i) 'SEQUENCE CHARACTERISTICS: LENGTH: 7 amino acids (A) (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: Met Glu Glu Lys Leu Lys Ala INFORMATION FOR SEQ ID NO:28: (2) SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 7 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown TOPOLOGY: unknown (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: Met Glu Glu Lys Met Lys Ala 5 INFORMATION FOR SEQ ID NO:29: (2) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: (B) STRAIN: E. coli (G) CELL TYPE: DH5 alpha IMMEDIATE SOURCE: (B) CLONE: C15 FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2..151
 (D) OTHER INFORMATION: /function= "synthetic" storage protein" /product= "protein" /gene= "ssp" /standard_name= "5.7.7.7.7.5" SEQUENCE DESCRIPTION: SEQ ID NO:29: C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met 10 GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu 20 25 AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met 35 160 AAG GCG TGATAGGTAC CG INFORMATION FOR SEQ ID NO:30: SEQUENCE CHARACTERISTICS: LENGTH: 49 amino acids TYPE: amino acid (B) TOPOLOGY: linear (D) (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

(ii)

(vi)

(vii)

(ix)

(xi)

Lys Ala

(2)

50

(i)

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu 1.0

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys 20 25

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys 35 40 45

Ala

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: C20
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..151
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
- C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG

 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met

 1 5 10 15
- GAG GAG AAG CTG AAG GCG ATG GAG GAG GAG CTG AAG GCG ATG GAG GAG 94
 Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
 20 25 30
- AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met 35 40 45

AAG GCG TGATAGGTAC CG Lys Ala 160

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

	()	ki)	SEQU	JENCE	E DES	SCRII	OITS	vi: 5	SEQ I	ID NO	0:32	:				
Met 1	Glu	Glu	Lys	Met 5	Lys	Ala	Met	Glu	Glu 10	Lys	Leu	Lys	Ala	Met 15	Glu	
Glu	Lys	Leu	Lys 20	Ala	Met	Glu	Glu	Lys 25	Leu	Lys	Ala	Met	Glu 30	Glu	Lys	
Leu	Lys	Ala 35	Met	Glu	Glu	Lys	Leu 40	Lys	Ala	Met	Glu	Glu 45	Lys	Met	Lys	
Ala																
(2)	11	NFORI	MATIC	ON FO	OR SI	EQ II	ои с	:33:								
		(i)	SE (A (B (C) LI) T) S	CE C ENGTE (PE: FRANI DPOLO	H: : nuc DEDNI	139 l Cleio ESS:	ISTI base c ac: dom near	pair	rs						
	1	(ii)	МО	LECU	LE T	YPE:	DN	A (g	enom	ic)						
	ı	(vi)	(B) S.	AL S FRAII LL T	N: 1	Ξ. c	oli 5 al	pha							
	(1	vii)			ATE LONE		CE:									
		(ix)	(A (B) L(AME/I	ION:		S .130 TION	: /:	st /p /g /s	tion orag rodu ene= tand .7.7	e processor e proc	otei: "pro p" name	n" tein	17	
		(xi)	SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID	NO:3	3:				
			AG A						lu G					la M		46
			CTG Leu												GAG Glu	94
			GCG Ala 35									TAGG	TAC	CG		139

- INFORMATION FOR SEQ ID NO:34: (2)
 - SEQUENCE CHARACTERISTICS:
 - LENGTH: 42 amino acids (A)
 - TYPE: amino acid (B)
 - (D) TOPOLOGY: linear
 - MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu 5 10

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys 20

Leu Lys Ala Met Glu Glu Lys Met Lys Ala

- INFORMATION FOR SEQ ID NO:35: (2)
 - SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - IMMEDIATE SOURCE: (vii)
 - (B) CLONE: D16
 - FEATURE: (ix)
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..88
 - (D) OTHER INFORMATION: /function= "synthetic storage protein" /product= "protein" /gene= "ssp" /standard name= "5.5.5.5"
 - SEQUENCE DESCRIPTION: SEQ ID NO:35: (xi)
- C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met 10 1
- GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala 20 25

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu

1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala 20 25

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: D20
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..109
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
- C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG

 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met

 1 5 10 15
- GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG GAA GAG 94
 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu
 20 25 30

AAG ATG AAG GCG TGATAGGTAC CG Lys Met Lys Ala

118

- INFORMATION FOR SEQ ID NO:38: (2)
 - SEQUENCE CHARACTERISTICS:
 - LENGTH: 35 amino acids (A)
 - TYPE: amino acid (B)
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu 5 10

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys 25 20

Met Lys Ala 35

- INFORMATION FOR SEQ ID NO:39: (2)
 - SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - MOLECULE TYPE: DNA (genomic) (ii)
 - ORIGINAL SOURCE: (vi)
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - IMMEDIATE SOURCE: (vii)
 - (B) CLONE: D33
 - (ix) FEATURE:

(xi)

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..88
- (D) OTHER INFORMATION: /function= "synthetic storage protein" /product= "protein"

/gene= "ssp" /standard name= "5.5.5.5"

- SEQUENCE DESCRIPTION: SEQ ID NO:39:
- C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met 5 10
- GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala 20

97

		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
		(ii)	MOLECULE TYPE: protein
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:40:
1	Met 1	Glu Glu	Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Gl 5 10 15
(Glu	Lys Met	Lys Ala Met Glu Glu Lys Met Lys Ala 20 25
	(2)	INFOR	MATION FOR SEQ ID NO:41:
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
		(ii)	MOLECULE TYPE: DNA (genomic)
		(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 121 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 86"
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:41:
	GAT	GGAGGAG .	AAGCTGAAGA A 21
	(2)	INFOR	MATION FOR SEQ ID NO:42:
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
		(ii)	MOLECULE TYPE: DNA (genomic)
		(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 121 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 87"
			120

CG

(2)

INFORMATION FOR SEQ ID NO:40:

(xi)	SEQUENCE DESCRIPTION: SEQ ID	NO:42:
ATCTTCTTCA	GCTTCTCCTC C	21
(2) INFOR	RMATION FOR SEQ ID NO:43:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(ix)	(A) NAME/KEY: misc_feature(B) LOCATION: 121(D) OTHER INFORMATION: /pr	
(xi)	SEQUENCE DESCRIPTION: SEQ ID	NO:43:
GATGGAGGAG	AAGCTGAAGT G	21
(2) INFO	RMATION FOR SEQ ID NO:44:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(ix)	(A) NAME/KEY: misc_feature(B) LOCATION: 121(D) OTHER INFORMATION: /pr	roduct= "synthetic oligonucleotide" /standard_name= "SM 89"
(xi)	SEQUENCE DESCRIPTION: SEQ ID	NO:44:
ATCCACTTCA	GCTTCTCCTC C	21
(2) INFO	RMATION FOR SEQ ID NO:45:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

(ix)	FEATURE: (A) NAME/KEY: misc_feat (B) LOCATION: 121 (D) OTHER INFORMATION:	/product= "synthetic oligonucleotide" /standard_name= "SM 90"
(xi)	SEQUENCE DESCRIPTION: SEQ	Q ID NO:45:
GATGGAGGAG	AAGATGAAGA A	21
(2) INFOR	MATION FOR SEQ ID NO:46:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pai (B) TYPE: nucleic acid (C) STRANDEDNESS: singl (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genor	nic)
(ix)	FEATURE: (A) NAME/KEY: misc_feat (B) LOCATION: 121 (D) OTHER INFORMATION:	ture /product= "synthetic oligonucleotide" /standard_name= "SM 91"
(xi)	SEQUENCE DESCRIPTION: SEC	Q ID NO:46:
ATCTTCTTCA	TCTTCTCCTC C	21
(2) INFOR	RMATION FOR SEQ ID NO:47:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base particles: (B) TYPE: nucleic acid (C) STRANDEDNESS: singuing (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genor	mic)
(ix)	FEATURE: (A) NAME/KEY: misc_feat (B) LOCATION: 121 (D) OTHER INFORMATION:	ture /product= "synthetic oligonucleotide" /standard_name= "SM 92"
(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO:47:
GATGGAGGAG	AAGATGAAGT G	21

- (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: LENGTH: 21 base pairs (A) TYPE: nucleic acid (B) (C) STRANDEDNESS: single TOPOLOGY: linear (D) (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: NAME/KEY: misc_feature (A) LOCATION: 1..21 (B) (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard name= "SM (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48: 21 ATCCACTTCA TCTTCTCCTC C INFORMATION FOR SEQ ID NO:49: (2) SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 7 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown TOPOLOGY: unknown (D) (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49: Met Glu Glu Lys Leu Lys Lys INFORMATION FOR SEQ ID NO:50: (2) SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 7 amino acids (B) TYPE: amino acid STRANDEDNESS: unknown (C) (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50: Met Glu Glu Lys Leu Lys Trp 1 5
- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Glu Lys Met Lys Lys
1 5

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Glu Lys Met Lys Trp 1 5

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 82-4
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..151
 - (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /gene= "ssp"

/standard_name=
"7.7.7.7.7.5"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
- C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG

 Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met

 1 5 10 15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
20 25 30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met 35 40 45

AAG GCG TGATAGGTAC CG Lys Ala 160

50

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu 1 5 10 15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
35 40 45

Ala

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 84-H3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..88
 - (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein"

/gene= "ssp"
/standard_name=
"5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met

1 5 10 15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
20 25

CG 97

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu

1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala 20 25

- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 86-H23
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..88
 - (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /gene= "ssp"

/standard name= "5.8.8.5"

SEQUENCE DESCRIPTION: SEQ ID NO:57: (xi)

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG AAG ATG Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met 10

GAG GAG AAG CTG AAG AAG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala 20 25

CG 97

- INFORMATION FOR SEQ ID NO:58: (2)
 - SEQUENCE CHARACTERISTICS:
 - LENGTH: 28 amino acids
 - TYPE: amino acid (B)
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met Glu 5 10

Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala

- (2) INFORMATION FOR SEQ ID NO:59:
 - SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 base pairs

 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - MOLECULE TYPE: DNA (genomic) (ii)
 - ORIGINAL SOURCE: (vi)
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 88-2
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..103
 - (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /gene= "ssp" /standard name= "5.9.9.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

C ATG GAG GAG AAG ATG AAG GCG AAG AAG CTG AAG TGG ATG GAG GAG

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu

1 5 10 15

AAG CTG AAG TGG ATG GAG GAG AAG CTG AAG TGG ATG GAA GAG AAG ATG 94 Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met

20 25 30

AAG GCG TGATAGGTAC CG Lys Ala 112

- (2) INFORMATION FOR SEQ ID NO:60:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu Lys

1 10 15

Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys
20 25 30

Ala

- (2) INFORMATION FOR SEQ ID NO:61:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 90-H8
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..109
 - (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /qene= "ssp"

/standard_name=
"5.10.10.10.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG AAG ATG Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Met

1 5 10 15

AAG ATG AAG GCG TGATAGGTAC CG Lys Met Lys Ala 118

- (2) INFORMATION FOR SEQ ID NO:62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met Glu 1 5 10 15

Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu Lys $20 \\ 25 \\ 30$

Met Lys Ala

- (2) INFORMATION FOR SEQ ID NO:63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 92-2
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..88

(D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /gene= "ssp" /standard_name= "5.11.11.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG TGG ATG

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met

1 5 10 15

CG 97

- (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met Glu
1 5 10 15

Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala 20 25

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 96"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGGAGGA AAGATGAAGG CGATGGAGGA GAAAATGAAA GCTATGGAGG AAAAGATGAA 60

AGCGAT	rggag gagaaaatga	AGGC	84
(2)	INFORMATION FOR	SEQ ID NO:66:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..84
 - (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 97"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

 ATCGCCTTCA TTTTCTCCTC CATCGCTTTC ATCTTTTCCT CCATAGCTTT CATTTTCTCC 60

 TCCATCGCCT TCATCTTTC CTCC 84
- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /label= name /note= "(SSP 5)4"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu

1 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala 20 25

- (2) INFORMATION FOR SEQ ID NO:68:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:	
	(A) NAME/KEY: misc_feature	
	(B) LOCATION: 184	
	(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"	
	/standard name= "SM	
	98"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
GATGGAGGA	A AAGCTGAAAG CGATGGAGGA GAAACTCAAG GCTATGGAAG AAAAGCTTAA 6	0
AGCGATGGA	G GAGAAACTGA AGGC 8	4
(2) INF	ORMATION FOR SEQ ID NO:69:	
(i) SEQUENCE CHARACTERISTICS:	
(+	(A) LENGTH: 84 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(ix	r) FEATURE:	
	(A) NAME/KEY: misc_feature	
	(B) LOCATION: 184	
	(D) OTHER INFORMATION: /product= "synthetic	
	oligonucleotide"	
	/standard_name= "SM 99"	
	99"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
ATCGCCTTC	A GTTTCTCCTC CTACGCTTTA AGCTTTTCTT CCATAGCCTT GAGTTTCTCC 6	0
ТССАТСССТ	T TCAGCTTTTC CTCC 8	4
1001110001		
(2) INF	ORMATION FOR SEQ ID NO:70:	
(2	\ CHOURNOR GUADAGERICO.	
(i	.) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: unknown	
	(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: protein	
(ix	c) FEATURE:	
(IX	(A) NAME/KEY: Protein	
	(B) LOCATION: 128	
	(D) OTHER INFORMATION: /label= name	
	/note= "(SSP 7)4"	
(xi	SEQUENCE DESCRIPTION: SEQ ID NO:70:	

(ii) MOLECULE TYPE: DNA (genomic)

Met 1	Glu	Glu	Lys	Leu 5	Lys	Ala	Met	Glu	Glu 10	Lys	Leu	Lys	Ala	Met 15	Glu	
Glu	Lys	Leu	Lys 20	Ala	Met	Glu	Glu	Lys 25	Leu	Lys	Ala					
(2)	II	1FORI	ITAN	ON F	OR S	EQ II	D NO	:71:								
		(i)	SEQI (A) (B) (C) (D)	L T S	E CH. ENGT: YPE: TRAN	H: nu DEDN	84 b clei ESS:	ase j c ac si:	pair: id ngle	S						
	(:	ii)	MOL	ECUL	E TY	PE:	DNA	(ge	nomi	c)						
	(:	ix)	(A) (B)	L	: IAME/ IOCAT THER	: NOI	1.	.84		prod ol	igon tand	ucle	nthe otid name	e"	М	
	(:	xi)	SEQ	UENC	E DE	SCRI	PTIO	N:	SEQ	ID N	0:71	:				
GAT	GGAG	GAA A	AAGC	TTAA	GA A	GATG	GAAG	A AA	AGCT	GAAA	TGG	ATGG	AGG	AGAA	ACTCAA	60
AAA	GATG	GAG (GAAA	AGCT	TA A	ATG										84
(2)	I	NFOR	MATI	ON F	OR S	EQ I	D NO	:72:								
		(i)	SEQ (A) (B) (C) (D)	I. T S	CE CH LENGT TYPE: STRAN	H: nu DEDN	84 b clei ESS:	ase c ac si	pair id ngle							
	(ii)	MOL	ECUL	E TY	PE:	DNA	. (ge	nomi	c)						
	(ix)	FEA (A) (B) (D)	I.	E: JAME/ JOCAT DTHER	: NOI	1.	.84		prod ol /s	igon	ucle	nthe otid	e"	M	
	(xi)	SEQ	UENC	CE DE	SCRI	PTIO	N:	SEQ	ID N	0:72	:				
ATC	CATT	TAA	GCTT	TTCC	CTC C	TACT	TTTT	'G AG	TTTC	TCCT	CCA	TCCA	TTT	CAGC	TTTTCT	60
TCC	'ATCT	TCT	TAAG	ירייויין	רדכ כ	ידיכיכי										84
						.100										0.1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

TOPOLOGY: unknown (D) (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73: Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp INFORMATION FOR SEQ ID NO:74: (2) SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) (ii) ORIGINAL SOURCE: (vi) (B) STRAIN: E. coli (G) CELL TYPE: DH5 alpha IMMEDIATE SOURCE: (vii) (B) CLONE: 2-9 FEATURE: (ix) (A) NAME/KEY: CDS (B) LOCATION: 2..235 (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /gene= "ssp" /standard name= "7.7.7.7.7.8.9.8.9.5" SEQUENCE DESCRIPTION: SEQ ID NO:74: (xi) 46 C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu 2.0 25 AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA AAG CTT 142 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu 35 40 AAG AAG ATG GAA GAA AAG CTG AAA TGG ATG GAG GAG AAA CTC AAA AAG 190 Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys

TYPE: amino acid

STRANDEDNESS: unknown

(B)

(C)

50

ATG GAG GAA AAG CTT AAA TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 242
Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala
65 70 75

C 243

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu

1 10 15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys 20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys 35 40 45

Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Met 50 55 60

Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala 65 70 75

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 5-1
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..172
 - (D) OTHER INFORMATION: /function= "synthetic storage protein /product= "protein" /gene= "ssp"

/standard_name= "5.5.5.7.7.7.5"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
- C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG

 Met Glu Glu Lys Met Lys Ala Met

 1 5 10 15
- GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG 94
 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
 20 25 30

AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG 142 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu 35 40 45

AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG Lys Ala Met Glu Glu Lys Met Lys Ala 50 55 179

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu

1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
35 40 45

Ala Met Glu Glu Lys Met Lys Ala 50 55

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha

- (ix) FEATURE: (A) NAME/KEY: CDS LOCATION: 3..173 (B) OTHER INFORMATION: /function= "synthetic (D) storage protein /product= "protein" /gene= "ssp" /standard_name= "SSP-3-5" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: CC ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 47 Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met 10 GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 95 Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu 25 20 AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA AAG ATG Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met 40 AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CGAATTC 187 Lys Ala Met Glu Glu Lys Met Lys Ala INFORMATION FOR SEQ ID NO:79: SEQUENCE CHARACTERISTICS: LENGTH: 56 amino acids TYPE: amino acid (B) (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:79: (xi) Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu 1 Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys 40 Ala Met Glu Glu Lys Met Lys Ala
- INFORMATION FOR SEQ ID NO:80: (2)

(2)

- SEQUENCE CHARACTERISTICS:
 - LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - TOPOLOGY: linear (D)

	(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 161	
		(B) LOCATION: 161 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 107"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:80:	
CATGG	AGGAG	AAGATGAAAA AGCTCGAAGA GAAGATGAAG GTCATGAAGT GATAGGTACC	60
G			61
(2)	INFOR	MATION FOR SEQ ID NO:81:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 61 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 161 (D) OTHER INFORMATION: /product= "synthetic ligonucleotide" /standard_name= "SM 106"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:81:	
AATTC	GGTAC	CTATCACTTC ATGACCTTCA TCTTCTCTTC GAGCTTTTTC ATCTTCTCCT	60
С			61
(2)	INFOR	MATION FOR SEQ ID NO:82:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: protein	
	(ix)	FEATURE: (A) NAME/KEY: Protein (B) LOCATION: 116 (D) OTHER INFORMATION: /label= name	

(ii) MOLECULE TYPE: DNA (genomic)

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:82:	
Met Glu Glu 1	Lys Met Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys 5 10 15	
(2) INFOR	MATION FOR SEQ ID NO:83:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 163 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 110"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:83:	
GCTGGAAGAA	AAGATGAAGG CTATGGAGGA CAAGATGAAA TGGCTTGAGG AAAAGATGAA	. 60
GAA		63
(2) INFOR	MATION FOR SEQ ID NO:84:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 163 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard_name= "SM 111"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:84:	
AGCTTCTTCA	TCTTTTCCTC AAGCCATTTC ATCTTGTCCT CCATAGCCTT CATCTTTTCT	6
TCC		6

- (2) INFORMATION FOR SEQ ID NO:85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
1 5 10 15

Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Leu Glu Glu Lys
20 25 30

Met Lys Val Met Lys
35

- (2) INFORMATION FOR SEQ ID NO:86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu 1 5 10 15

Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Leu Glu Glu Lys
20 25 30

Met Lys Val Met Lys 35

- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: /product= "synthetic oligonucletide"

/standard_name= "SM 112"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
GCTCGAAGAA AGATGAAGGC AATGGAAGAC AAAATGAAGT GGCTTGAGGA GAAAATGAAG 6	50
AA	52
(2) INFORMATION FOR SEQ ID NO:88:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 62 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 162 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
AGCTTCTTCA TTTTCTCCTC AAGCCACTTC ATTTTGTCTT CCATTGCCTT CATCTTTCTT 6	50
CG	52
(2) INFORMATION FOR SEQ ID NO:89:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 37 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys 1 10 15	
Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys 20 25 30	
Met Lys Val Met Lys 35	
(2) INFORMATION FOR SEQ ID NO:90:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: NAME/KEY: misc_feature (A) (B) LOCATION: 1..63 OTHER INFORMATION: /product= "synthetic (D) oligonucleotide" /standard_name= "SM 114" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90: GCTCAAGGAG GAAATGGCTA AGATGAAAGA CGAAATCTGG AAACTGAAAG AGGAAATGAA 60 63 INFORMATION FOR SEQ ID NO:91: SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs TYPE: nucleic acid STRANDEDNESS: single (C) TOPOLOGY: linear (D) MOLECULE TYPE: DNA (genomic) (ii) FEATURE: (ix) (A) NAME/KEY: misc_feature (B) LOCATION: 1..63 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide" /standard name= "SM 115" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91: AGCTTCTTCA TTTCCTCTTT CAGTTTCCAC ATTTCGTCTT TCATCTTAGC CATTTCCTCC 60 63 INFORMATION FOR SEQ ID NO:92: (i) SEQUENCE CHARACTERISTICS: LENGTH: 107 amino acids TYPE: amino acid (B) (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92: Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys 10 Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys 20 25

GAA

(2)

TTG

(2)

Met Lys Val Met Glu Glu Lys Met Lys Leu Glu Glu Lys Met Lys

35 40 45

Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu 50 60

Glu Glu Lys Met Lys Val Met Glu Glu Lys Met Lys Leu Glu Glu 65 70 75 80

Lys Met Lys Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met 85 90 95

Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys 100 105

- (2) INFORMATION FOR SEQ ID NO:93:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 839 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

- (2) INFORMATION FOR SEQ ID NO:94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:94:	
CTAGAAGCCT C	GGCAACGTC AGCAACGGCG GAAGAATCCG GTG 43	
(2) INFORM	ATION FOR SEQ ID NO:95:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:95:	
CATGCACCGG A	TTCTTCCGC CGTTGCTGAC GTTGCCGAGG CTT 43	
(2) INFORM	NATION FOR SEQ ID NO:96:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:96:	
GATCCCATGG C	CGCCCTTAA GTCCACCGCC AGCCTCCCCG TCGCCCGCCG CTCCT	55
(2) INFORM	MATION FOR SEQ ID NO:97:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 55 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:97:	
CTAGAGGAGC C	GGCGGGCGAC GGGGAGGCTG GCGGTGGACT TAAGGGGCGC CATGG	55
(2) INFORMA	ATION FOR SEQ ID NO:98:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 59 base pairs (B) TYPE: nucleic acid	

TYPE: nucleic acid

(B)

16

- (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) (ii) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98: CATGGCGCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC INFORMATION FOR SEQ ID NO:99: SEQUENCE CHARACTERISTICS: LENGTH: 59 base pairs (A) TYPE: nucleic acid (B) STRANDEDNESS: single (C) (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:99: (xi) TTAAGCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC INFORMATION FOR SEQ ID NO:100: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs (A) TYPE: nucleic acid (B) STRANDEDNESS: single (C) TOPOLOGY: linear (D) (ii) MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:100: (xi) GCGCCCACCG TGATGA 16 INFORMATION FOR SEQ ID NO:101: SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs TYPE: nucleic acid (B) STRANDEDNESS: single (C) (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
- INFORMATION FOR SEQ ID NO:102: (2)

59

(2)

59

(2)

(2)

(i)

CACCGGATTC TTCCGC

- SEQUENCE CHARACTERISTICS: (i)
 - LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid

		(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:102:	
5	GTAAGATTGG	TAAAGTCCAG CAAGAAAATG AGATAAAAGA GAAGCCTGAA ATGACGAAAA	60
	AATCAGGTGT	TTTGATTCTT GGTGCTGGAC GTGTGTNTCG CCCAGCTGCT GATTTCCTAG	120
	CTTCAGTTAG	AACCATTTCG TCACAGCAAT GGTACAAAAC ATATTTCGGA GCAGACTCTG	180
10	AAGAGAAAAC	AGATGTTCAT GTGATTGTCG CGTCTCTGTA TCTTAAGGAT GCCAAAGAGA	240
	CGGTTGAAGG	TATTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT AGTGAAAGTC	300
15	TCCTTAAGTA	TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA AGTTGTCATG	360
15	CTTGTTGTAG	CA	372
	(2) INFO	RMATION FOR SEQ ID NO:103:	
20	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
25	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:103:	
25	GGAAGCACAC	TGCGACTCTT TTGGAATTCG GGGACATCAA GAATGGACAA ACAACAACCG	60
	CTATGGCCAA	GACTGTTGGG ATCCCTGCAG CCATTGGAGC TCTGCTGTTA ATTGAAGACA	120
30	AGATCAAGAC	AAGAGGAGTC TTAAGGCCTC TCGAAGCAGA GGTGTATTTG CCAGCTTTGG	180
	ATATATTGCA	AGCATATGGT ATAAAGCTGA TGGAGAAGGC AGAATGATCA AAGAACTCTG	240
35	TATATTGTTT	CTNTCTATAA CTTGGAGTTG GAGACAAAGC TGAAGGAGNC AGNGCCATTA	300
	GACCAGCAAA	AAAAGGAGGA GGA	323
	(2) INFO	RMATION FOR SEQ ID NO:104:	
40	(i) (ii)	(A) LENGTH: 123 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

	(xi)		i)	SEQUENCE DESCRIPTION: SEQ ID NO:104:												
5	Lys 1	Ile	Gly	Lys	Val 5	Gln	Gln	Glu	Asn	Glu 10	Ile	Lys	Glu	Lys	Pro 15	Glu
3	Met	Thr	Lys	Lys 20	Ser	Gly	Val	Leu	11e 25	Leu	Gly	Ala	Gly	Arg 30	Val	Xaa
10	Arg	Pro	Ala 35	Ala	Asp	Phe	Leu	Ala 40	Ser	Val	Arg	Thr	Ile 45	Ser	Ser	Gln
	Gln	Trp 50	Tyr	Lys	Thr	Tyr	Phe 55	Gly	Ala	Asp	Ser	Glu 60	Glu	Lys	Thr	Asp
15	Val 65	His	Val	Ile	Val	Ala 70	Ser	Leu	Tyr	Leu	Lys 75	Asp	Ala	Lys	Glu	Thr 80
20	Val	Glu	Gly	Ile	Ser 85	Asp	Val	Glu	Ala	Val 90	Arg	Leu	Asp	Val	Ser 95	Asp
20	Ser	Glu	Ser	Leu 100	Leu	Lys	Tyr	Val	Ser 105	Gln	Val	Asp	Val	Val 110	Leu	Ser
25	Leu	Leu	Pro 115	Ala	Ser	Cys	His	Ala 120	Cys	Cys	Ser					
	(2)	II	NFOR	TAM	ON F	OR S	EQ I	D NO	:105	:						
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 74 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 															
30		(ii)	(D)												
	(ii) MOLECULE TYPE: protein(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:															
35	Lys 1	His	Thr	Ala	Thr 5	Leu	Leu	Glu	Phe	Gly 10	Asp	[Ile	Lys	Asn	Gly 15	Gln
40	Thr	Thr	Thr	Ala 20	Met	Ala	Lys	Thr	Val 25	Gly	Ile	Pro	Ala	Ala 30	Ile	Gly
	Ala	Leu	Leu 35	Leu	Ile	Glu	Asp	Lys 40	Ile	Lys	Thr	Arg	Gly 45	Val	Leu	Arg
45	Pro	Leu 50	Glu	Ala	Glu	Val	Tyr 55	Leu	Pro	Ala	Leu	Asp	Ile	Leu	Gln	Ala

50 INFORMATION FOR SEQ ID NO:106: (2)

65

(i) SEQUENCE CHARACTERISTICS:

Tyr Gly Ile Lys Leu Met Glu Lys Ala Glu 70

- (A) LENGTH: 25 base pairs
- TYPE: nucleic acid (B)

		(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
5	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:106:	
	ATTCCCCATG	GTTTCGCCGA CGAAT	25
	(2) INFOR	RMATION FOR SEQ ID NO:107:	
10	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
15	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:107:	
1)	amamaaam» a	CTA CTA CCTA CTCA TCA A C	20